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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/400,492

DATE: 10/06/1999
TIME: 09:26:28

Input Set: I400492.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Rhodes, Kenneth
2 An, Wenqian
3 <120> TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
4 <130> FILE REFERENCE: MNI-069CP
5 <140> CURRENT APPLICATION NUMBER: US/09/400,492
6 <141> CURRENT FILING DATE: 1999-09-21
7 <150> EARLIER APPLICATION NUMBER: USSN 60/110,277
8 <151> EARLIER FILING DATE: 1998-11-30
9 <150> EARLIER APPLICATION NUMBER: USSN 60/110,033
10 <151> EARLIER FILING DATE: 1998-11-25
11 <150> EARLIER APPLICATION NUMBER: USSN 60/109,333
12 <151> EARLIER FILING DATE: 1998-11-20
13 <150> EARLIER APPLICATION NUMBER: USSN 09/298,731
14 <151> EARLIER FILING DATE: 1999-04-23
15 <150> EARLIER APPLICATION NUMBER: USSN 09/350,614
16 <151> EARLIER FILING DATE: 1999-07-09
17 <150> EARLIER APPLICATION NUMBER: USSN 09/350,874
18 <151> EARLIER FILING DATE: 1999-07-09
19 <160> NUMBER OF SEQ ID NOS: 73
20 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO 1
22 <211> LENGTH: 1463
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (225)..(872)
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31 tttctctctc tccaattcag agtagacaaa ccacggggat ttctttccag ggtagggggag 180
32 gggccggggc cggggtccca actcgcactc aagtcttcgc tgcc atg ggg gcc gtc 236
33 Met Gly Ala Val
34 1
35 atg ggc acc ttc tca tct ctg caa acc aaa caa agg cga ccc tcg aaa 284
36 Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg Arg Pro Ser Lys
37 5 10 15 20
38 gat aag att gaa gat gag ctg gag atg acc atg gtt tgc cat cgg ccc 332
39 Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys His Arg Pro
40 25 30 35
41 gag gga ctg gag cag ctc gag gcc cag acc aac ttc acc aag agg gag 380
42 Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Glu
43 40 45 50
44 ctg cag gtc ctt tat cga ggc ttc aaa aat gag tgc ccc agt ggt gtg 428

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47      gtc aac gaa gac aca ttc aag cag atc tat gct cag ttt ttc cct cat      476
48      Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His
49              70                      75                      80
50      gga gat gcc agc acg tat gcc cat tac ctc ttc aat gcc ttc gac acc      524
51      Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr
52              85                      90                      95                      100
53      act cag aca ggc tcc gtg aag ttc gag gac ttt gta acc gct ctg tcg      572
54      Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser
55              105                      110                      115
56      att tta ttg aga gga act gtc cac gag aaa cta agg tgg aca ttt aat      620
57      Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn
58              120                      125                      130
59      ttg tat gac atc aac aag gac gga tac ata aac aaa gag gag atg atg      668
60      Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met
61              135                      140                      145
62      gac att gtc aaa gcc atc tat gac atg atg ggg aaa tac aca tat cct      716
63      Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro
64              150                      155                      160
65      gtg ctc aaa gag gac act cca agg cag cat gtg gac gtc ttc ttc cag      764
66      Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln
67      165                      170                      175                      180
68      aaa atg gac aaa aat aaa gat ggc atc gta act tta gat gaa ttt ctt      812
69      Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu
70              185                      190                      195
71      gaa tca tgt cag gag gac gac aac atc atg agg tct ctc cag ctg ttt      860
72      Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu Phe
73              200                      205                      210
74      caa aat gtc atg taactggtga cactcagcca ttcagctctc agagacattg      912
75      Gln Asn Val Met
76              215
77      tactaaacaa ccaccttaac acctgatct gcccttggtc tgattttaca caccaactct 972
78      tgggacagaa acacctttta cactttggaa gaattctctg ctgaagactt tcttatggaa 1032
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80      agacaagatg aaatttgagt ttgttttga agcatgctca tctcctcaca ctgctgccct 1152
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84      gtgggaagaa tgagagttat ccagaacaat taggatctgt catgaccaga ttgggagagc 1392
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86      aaactgcccc g      1463
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89      <212> TYPE: PRT
90      <213> ORGANISM: Homo sapiens
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94      Arg Pro Ser Lys Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val

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96  Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
97          35          40          45
98  Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
99          50          55          60
100 Pro Ser Gly Val Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln
101          65          70          75          80
102 Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
103          85          90          95
104 Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
105          100          105          110
106 Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg
107          115          120          125
108 Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
109          130          135          140
110 Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
111          145          150          155          160
112 Tyr Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp
113          165          170          175
114 Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
115          180          185          190
116 Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser
117          195          200          205
118 Leu Gln Leu Phe Gln Asn Val Met
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123 <213> ORGANISM: Rattus sp.
124 <220> FEATURE:
125 <221> NAME/KEY: CDS
126 <222> LOCATION: (300)..(1034)
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130  ggggaaataa aagcaaagat taccatgaat tgcaagatta cctagcaatt gcaaggtagg 180
131  aggagagagg tggagggcgg agtagacagg agggagggag aaagtgagag gaagctaggc 240
132  tggtggaat aaccctgcac ttggaacagc ggcaaagaag cgcgattttc cagctttaa 299
133  atg cct gcc cgc gtt ctg ctt gcc tac ccg gga acg gag atg ttg acc 347
134  Met Pro Ala Arg Val Leu Leu Ala Tyr Pro Gly Thr Glu Met Leu Thr
135  1          5          10          15
136  cag ggc gag tct gaa ggg ctc cag acc ttg ggg ata gta gtg gtc ctg 395
137  Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu
138  20          25          30
139  tgt tcc tct ctg aaa cta ctg cac tac ctc ggg ctg att gac ttg tcg 443
140  Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
141  35          40          45
142  gat gac aag atc gag gat gat ctg gag atg acc atg gtt tgc cat cgg 491
143  Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg
144  50          55          60

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146 Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
147 65 70 75 80
148 gaa ctg caa gtc ctt tac cgg gga ttc aaa aac gag tgc ccc agt ggt 587
149 Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
150 85 90 95
151 gtg gtt aac gaa gag aca ttc aag cag atc tac gct cag ttt ttc cct 635
152 Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro
153 100 105 110
154 cat gga gat gcc agc aca tac gca cat tac ctc ttc aat gcc ttc gac 683
155 His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp
156 115 120 125
157 acc acc cag aca ggc tct gta aag ttc gag gac ttt gtg act gct ctg 731
158 Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu
159 130 135 140
160 tcg att tta ctg aga gga acg gtc cat gaa aaa ctg agg tgg acg ttt 779
161 Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe
162 145 150 155 160
163 aat ttg tac gac atc aat aaa gac ggc tac ata aac aaa gag gag atg 827
164 Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met
165 165 170 175
166 atg gac ata gtg aaa gcc atc tat gac atg atg ggg aaa tac acc tat 875
167 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
168 180 185 190
169 cct gtg ctc aaa gag gac act ccc agg cag cac gtg gac gtc ttc ttc 923
170 Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe
171 195 200 205
172 cag aaa atg gat aaa aat aaa gat ggc att gta acg tta gac gaa ttt 971
173 Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe
174 210 215 220
175 ctc gag tcc tgt cag gag gat gac aac atc atg agg tct cta cag ctg 1019
176 Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu
177 225 230 235 240
178 ttc caa aat gtc atg taactgagga cactggccat cctgctctca gagacactga 1074
179 Phe Gln Asn Val Met
180 245
181 caaacacctc aatgcctga tctgcccttg ttccagtttt acacatcaac tctcgggaca 1134
182 gaaatacctt ttacactttg gaagaattct ctgctgaaga ctttctacaa aacctggcac 1194
183 cgagtggctc agtctctgat tgccaactct tctcctctcc tctcttgag agggacgagc 1254
184 tgaaatccga agtttgtttt ggaagcatgc ccatctctcc atgctgctgc tgccctgtgg 1314
185 aaggccccctc tgetttagct taaacagtag tgcacagttt tctgcgtata cagatcccca 1374
186 actcactgcc tctaagtcag gcagaccctg atcaatctga accaaatgtg caccatcctc 1434
187 cgatggcctc ccaagccaat gtgcctgctt ctcttctctt ggtgggaaga aagaacgctc 1494
188 tacagagcac ttagagctta ccatgaaaat actgggagag gcagcaccta acacatgtag 1554
189 aataggactg aattattaag catggtggta tcagatgatg caaacagccc atgtcatttt 1614
190 tttttccaga ggtagggact aataattctc ccacactagc acctacgac atagaacaag 1674
191 tcttttaaca catccaggag ggaaccgct gccagtggt ctatcccttc tctccatccc 1734
192 ctgctcaagc ccagcactgc atgtctctcc cggaaggtcc agaatgctg tgaatgctg 1794
193 taacttttat accctgttat aatcaataaa cagaactatt tcgtacaaaa aaaaaaaaaa 1854
194 aa 1856

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197 <212> TYPE: PRT
198 <213> ORGANISM: Rattus sp.
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202 Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu
203 20 25 30
204 Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
205 35 40 45
206 Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg
207 50 55 60
208 Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
209 65 70 75 80
210 Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
211 85 90 95
212 Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Pro
213 100 105 110
214 His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp
215 115 120 125
216 Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu
217 130 135 140
218 Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe
219 145 150 155 160
220 Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met
221 165 170 175
222 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
223 180 185 190
224 Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe
225 195 200 205
226 Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe
227 210 215 220
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235 <213> ORGANISM: Mus musculus
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239 <400> SEQUENCE: 5
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242 gcacgccggc cccgtgtcca acatcaggca ggctttgggg ctcggggctc gggcctcgga 180
243 gaagccagtg gcccggtcgt gtgcccgcac cggggggcgc ctgtgaaggc tcccgcgagc 240
244 ctctqccct gggagtcagt gcatgtgcct ggctgaagaa ggcagcagcc acgagctcca 300

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY
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DATE: 10/06/1999
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Line	? Error/Warning	Original Text
576	W "N" or "Xaa" used: Feature required	ggt aac gaa gag aca ttc aag cng atc tac g
615	W "N" or "Xaa" used: Feature required	Pro Ser Gly Val Val Asn Glu Glu Thr Phe L
809	W Invalid/Missing Amino Acid Numbering	
1993	W "N" or "Xaa" used: Feature required	cacccatgct ggcatactgt aattgcccac taaacaaa
2207	W "N" or "Xaa" used: Feature required	Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp L
2209	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Glu Phe Xaa Xaa Xaa Xaa